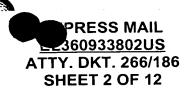


RESS MAIL
EL360933802US
ATTY. DKT. 266/186
SHEET 1 OF 12





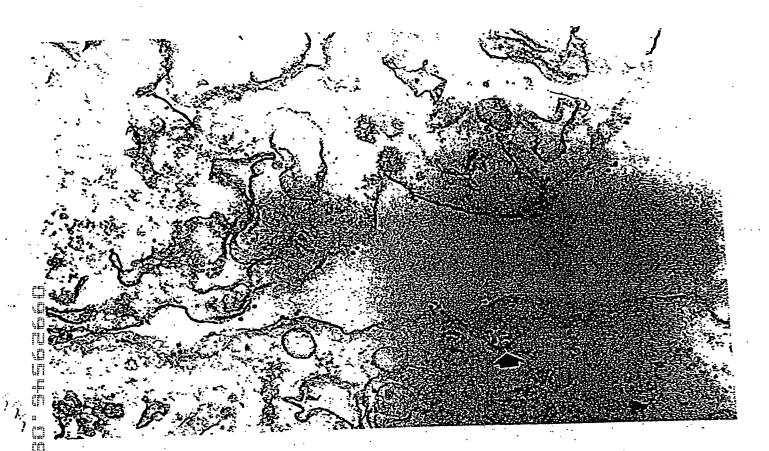


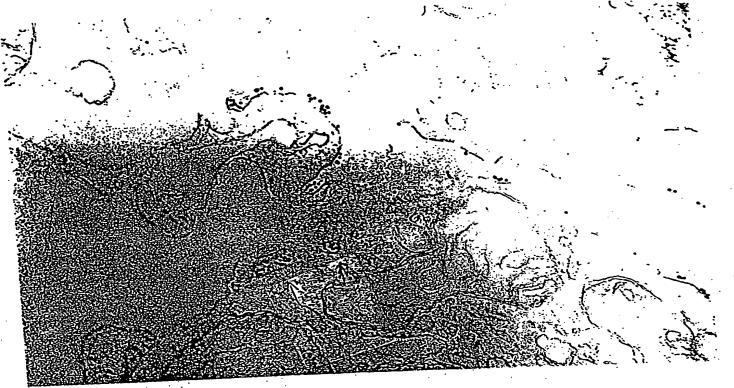
FIGURE 2





E...RESS MAIL <u>EL360933802US</u> ATTY. DKT. 266/186 SHEET 4 OF 12





EL369933802US ATTY. DKT. 266/186 SHEET 5 OF 12



EX. RESS MAIL <u>EL360933802US</u> ATTY. DKT. 266/186 SHEET 6 OF 12

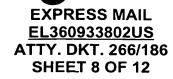
VH1E.SEQ(1>267)
VH3E.SEQ(1>264)
VH4E.SEQ(1>210)
VH1E.SEQ(1>115)
VH12UE.SEQ(1>130)
VH15UE.SEQ(1>130)
VH1FORE.SEQ(1>208)
VH3FORE.SEQ(1>207)
VH4FORE.SEQ(1>230)
VH4ESESEQ(1>131)
VH12E.SEQ(1>109)
VH1UE.SEQ(1>42)



EXPRESS MAIL 36093380<u>2US</u> ATTY. DKT. 266/186 **SHEET 7 OF 12**

All 74 enzymes (No Filter) Linear, Certain Siles Only, Slandard Genetic Code Enzymes: Settings: Ava II Sau96 I Sau96 IPvu II TCTCCTGTCAGGAACTGCAGGTGTCCTCTCTGAGGTCCAGCTGCAACAGTCTGGACCTGAACTGGTGAAG AGAGGACAGTCCTTGACGTCCACAGGAGACTCCAGGTCGACGTTGTCAGACCTGGACTTGACCACTTC SEQ. ID. NO. 1 SEQ. ID. NO. 2 SEVOLOGS CP SEQ. ID. NO. 3 V S S L R S S C N S L D L SCOELOY SEQ. ID. NO. 4 SEQ. ID. NO. 5 Bsr I Hph l ECORV CCTGGGACTTCAGTGAGGATATCCIGCAAGACTTCTGGATACACATTCACTGAATATACCATACACTGGG GGACCCTGAAGTCACTCCTATAGGACGTTCTGAAGACCIATGTGTAAGTGACTTATATGGTATGTGACCC SEQ. ID. NO. 1 WOFSEDILOOFWIHIH . I Y HIT LO GTSVR [SCKTSGYTFTEY TIMEN LGLO GYPARLLDTHSLN, I'PYT. G SEQ. ID. NO. 2 SEQ. ID. NO. 3 P G T. S SEQ. ID. NO. 4 SEQ. ID. NO. 5 . Kpn l TGAAGCAGAGCCATGGAAAGAGCCTTGAGTGGATTGGAAACATCCTAACAATGGTGGTACCACCTA ACTTCGTCTCGGTACCTTTCTCGGAACTCACCTAACCTTTGTAGTTAGGATTGTTACCACCATGGTGGAT SEQ. ID. NO. 1 EAEPWKEP VOWKHOS OWWY.H KOSHGKSLEWIGNINPNNGGT SRAHERALSGLETSILTHVVP SEQ. ID. NO. 2 SEQ. ID. NO. 3 SEQ. ID. NO. 4 / SEQ. ID. NO. 5 Ban II Saci Bsr I Rsa I Acci - 4 Hae III CAATCAGAAGTTCGAGGACAAGGCCACATTGACTGTAGACAAGTCCTCCAGTACAGCGTACATGGAGCTC GTTAGTCTTCAAGCTCCTGTTCCGGTGTAACTGACATCTGTTCAGGAGGTCATGTCGGATGTACCTCGAG SEQ. ID. NO. 1 SEVRGOGHIDEROVLOYSLHG NOKFEDKATLTVDKSSSTAYME IRSSRTRPH.L.T.SPPVOPT.W SEQ. ID. NO. 2 SEQ. ID. NO. 3 ·NOKF SEQ. ID. NO. 4 SEQ. ID. NO. 5 Sau96'l Bsr I Hae III Pvi II Dide I. Hinf.I CGCAGCCTAACATCTGAGGATTCTGCAGTCTATTATTGTGCAGCTGGTTGGAACTTTGACTAGTGGGGCC GCGTCGGATTGTAGACTCCTAAGACGTCAGATAATAACACGTCGACCAACCTTGAAACTGATGACCCCCGG SEQ. ID. NO. 1 SEQ. ID. NO. 2 POPNI GFCSLLLCSWLEL I RSLTSEDSAV-YYCAAGWNFD AA..HLRILOSIIVOLYGTLT SEQ. ID. NO. 3 SEQ. ID. NO. 4 G:T L T SEQ. ID. NO. AJw26 1 Ode I AAGGCACCACTCTCACAGTCTCCTCAGCCAAAACGACACCC TTCCGTGGTGAGAGTGTCAGAGGAGTCGGTTTTGCTGTGGG SEQ. ID. NO. 1 SEQ. ID. NO. 2 R H H S H S L L S Q H D T Q G T T L T Y S S A K T T K A P L S Q S P Q P K R H SEO. TD. NO. 3 SEQ. ID. NO. 4 SEQ. ID. NO. 5

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Lipman-Pearson Prot Ktuple: 2; Gap Pena Seq1(1>115)	ein Alignment Ity: 4, Gap Length I Seq2(1>125) MUVHIIA PRO	Penalty: 12 Similarity Index	Gap Number	Length L	ensus _ength
J591VH.PRO		75.6	2	10	125
(1>115) EVOLOGSGPELVKPO EVOLOGSGPELVKPO EVOLOGSGPELVKPO F70 YNOKFEDKATLTYD YNOKFKGKATLTYD	TSYRISCKTSGYTF SSY: ISCK: SGYTF ASYKISCKASGYTF 420 480	630 TEYTI-HWVKO T:Y::WVKO TOYYMNWVKO 430 630 680 680 680 680 680 680 680 680 680 68	SHGKSLEWIG S GKSLEWIG SPGKSLEWIG 40	*50 *60 *100 *11C WNFDYWGOGTT FNYWGOGTT	
					:

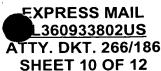
7

LTVSS :TVSS VTVSS



VK15E.SEQ(1>124)
VK16E.SEQ(1>118)
VK20E.SEQ(1>153)
VK27UE.SEQ(1>153)
VK18E.SEQ(1>153)
VK18E.SEQ(1>153)
VK26UE.SEQ(1>153)
VK26UE.SEQ(1>153)
VK25UE.SEQ(1>20)
VK15UE.SEQ(1>230)
VK15UE.SEQ(1>209)
VK18UE.SEQ(1>1442)
VK18UE.SEQ(1>80)





All 74 enzymes (No Filter) Linear, Certain Sites Only, Standard Genetic Code Hph I Enzymes: Settings: TTATATGGAGCTGATGGGAACATTGTAATGACCCAATCTCCCAAATCCATGTCCATGTCAGTAGGAGAGA SEQ. ID. NO. 10 AATATACCTCGACTACCCTTGTAACATTACTGGGTTAGGGGTTAGGTACAGGTACAGTCATCCTCTCT т и н т а в Р к в н в н T L PREPERCO.E

H C N D P I S Q I H Y H Y S R L Y G SEQ. ID. NO. 11 G SEQ. ID. NO. 12 ε SEQ. ID. NO. 13 GGGTCACCTIGACCTGCAAGGCCAGTGAGAATGTGGTTACTTATGTTTCCTGGTATCAACAGAAACCAGA SEQ. ID. NO. 10 CCCAGTGGAACTGGACGTTCCGGTCACTCTTACACCAATGAATACAAAGGACCATAGTTGTCTTTGGTCT SEQ. ID. NO. 9 SEQ. ID. NO. 11 SEQ. ID. NO. 12 SEQ. ID. NO. 13 Ava II Dpn I Bsa0 I Sau96 I Pvu I Rsa1 GCAGTCTCCTAAACTGCTGATATACGGGGCATCCAACCGGTACACTGGGGTCCCCGATCGCTTCACAGGC SEQ. ID. NO. 10 CGTCAGAGGATTTGACGACTATATGCCCCGTAGGTTGGCCATGTGACCCCAGGGGCTAGCGAAGTGTCCG Q S P K L L I Y C: A S N R Y T
S L L N C Y T G H P. T G T L
A V S . T A D I R G I . Q P Y H V PI SEQ. ID. NO. 11 SEQ. ID. NO. 12 SEQ. ID. NO. 13 Mbo II E∞57 I Bsp6 II Mbo1 Opn1 AGTGGATCTGCAACAGATTTCACTCTGACCATCAGCAGTGTGCAGGCTGAAGACCTTGCAGATTATCACT TEACCTAGACGTTGTCTAAAGTGAGACTGGTAGTCGTCACACGTCCGACTTCTGGAACGTCTAATAGTGA SEQ. ID. NO. 9. S G S A T O F T L T I S S V Q A E D L A D Y
V D. L Q Q I S L P S A V. C R L K T L Q I
Q W I C N R F H S O H Q O C A G . R P C R L · SEQ. ID. NO. 10 SEQ. ID. NO. 11 SEQ. ID. NO. 12 SEQ. ID. NO. 13 Ava II. Saugel Alul GTGGACAGGGTTACAGCTATCCGTACACGTTCGGAGGGGGGACCAAGCTGGAAATAAAACGGGCTGATGC 350 Rsa I CACCTGTCCCAATGTCGATAGGCATGTGCAAGCCTCCCCCCTGGTTCGACCTTTATTTTGCCCGACTACG SEQ. ID. NO. 9 Y P Y T F G G G T K L E I K R : R T R S E G G P S W K . N S V H V R R G D Q A G N K T SEQ. ID. NO. 10 V D R V T A V T G L O L SEQ. ID. NO. 11 SEQ. ID. NO. 12 SEQ. ID. NO. 13 TGCACCAACTGTA 363. SEQ. ID. NO. 9 ACGTGGTTGACAT SEQ. ID. NO. 10 A P. T. V SEQ. ID. NO. 11 SEQ. ID. NO. 12 SEQ. ID. NO. 13

(n Alignment /: 4; Gap Length I / Seq2(1>111) MUVKV.PRO	Penalty: 12 Similarity Index	Gap Number	Gap Length	Conser Le	nsus ngth
J591VK.PRO (1>107)	(1>109)	60.4	2 .	2	·.	109
#10 NIVMTOSPKSMSMSVGI :[MTOSP.S:S S:G DIOMTOSPSSLSASLG 4:0 #60 ORFIGSGSATOFTLTI .RE:GSGS:TD::LTI SRFSGSGSGTDYSLTI	RVIIICAS DRVTITCRASODO 20 80 SSVOAEDLADYHC	VTTYVSWYOOK YTTYVSWYOOK SNYLNWYOOK 30 490 GOGYSY-PYTF	PEOSPKLLIYO P. SPKLLIY PGGSPKLLIYY 40 *! • 100: GGGTKLEIK GGGTKLEIK	-50 ASNRYTGV AS: :GV (ASRLHSGV	16	

